

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: May 30, 2003, 13:03:28 ; Search time 495 Seconds

(without alignments)
10792.369 Million cell updates/sec

Title: US-08-153-397a-1
Perfect score: 3962

Sequence: 1 CGGGCTTGAGACTGGGGTGA.....AAAAAAMAAACCGGAATTC 3962

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	3638.6	91.8	3751	9 US-09-355-815-1	Sequence 1, Appl1
2	3613.4	91.2	3849	9 US-10-050-036-4549	Sequence 4549, Appl1
3	3451.4	87.1	3637	10 US-09-223-490-3	Sequence 3, Appl1
4	2783.6	70.3	2861	10 US-09-935-297-279	Sequence 279, Appl1
5	1192.2	30.1	1197	10 US-09-223-491-7	Sequence 7, Appl1
6	950.4	24.0	12010	10 US-09-880-107-3369	Sequence 3369, Appl1
7	642.0	16.2	3096	9 US-09-355-815-5	Sequence 5, Appl1
8	639.8	16.1	3120	9 US-09-158-72-19	Sequence 19, Appl1
9	522.8	13.2	563	10 US-09-815-343-505	Sequence 505, Appl1
10	361.4	9.1	2083	10 US-09-771-161A-14	Sequence 14, Appl1
11	301.8	7.6	305	9 US-10-060-036-2378	Sequence 2378, Appl1
12	301.8	7.5	305	9 US-10-060-036-4529	Sequence 4529, Appl1
13	284.8	7.2	289	10 US-09-234-093B-1691	Sequence 1691, Appl1
14	255.6	6.4	470	9 US-09-918-995-9027	Sequence 907, Appl1
15	232.8	5.9	387	10 US-09-900-352-726	Sequence 776, Appl1
16	230.4	5.8	231	10 US-09-598-599-591	Sequence 591, Appl1
17	220.4	5.8	463	10 US-09-864-761-1663	Sequence 1663, Appl1
18	198.8	5.0	489	9 US-09-918-995-10135	Sequence 10135, Appl1
19	184.2	4.6	465	10 US-09-887-701-1251	Sequence 1251, Appl1

ALIGNMENTS

SEQ ID NO	LENGTH:	TYPE: DNA	SEQUENCE
1	3751	ORGANISM: Homo sapiens	US-09-355-815-1
2	3751	US-09-355-815-1	Query Match 91.8%; Score 3638.6; DB 9; Length 3751;
3	3751	US-09-355-815-1	Best Local Similarity 98.9%; Pred. No. 0; Matchers 3733; Conservative 0; Mismatches 14; Indels 26; Gaps 6;
4	3751	US-09-355-815-1	Sequence 1, Appl1
5	3751	US-09-355-815-1	Sequence 4549, Appl1
6	3751	US-09-355-815-1	Sequence 3, Appl1
7	3751	US-09-355-815-1	Sequence 279, Appl1
8	3751	US-09-355-815-1	Sequence 7, Appl1
9	3751	US-09-355-815-1	Sequence 5, Appl1
10	3751	US-09-355-815-1	Sequence 19, Appl1
11	3751	US-09-355-815-1	Sequence 505, Appl1
12	3751	US-09-355-815-1	Sequence 14, Appl1
13	3751	US-09-355-815-1	Sequence 2378, Appl1
14	3751	US-09-355-815-1	Sequence 4529, Appl1
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21	3751	US-09-355-815-1	Sequence 1251, Appl1
22	3751	US-09-355-815-1	Sequence 4, Appl1
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27	3751	US-09-355-815-1	Sequence 4999, Appl1
28	3751	US-09-355-815-1	Sequence 18419, A
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31	3751	US-09-355-815-1	Sequence 2, Appl1
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33	3751	US-09-355-815-1	Sequence 1, Appl1
34	3751	US-09-355-815-1	Sequence 32, Appl1
35	3751	US-09-355-815-1	Sequence 128, Appl1
36	3751	US-09-355-815-1	Sequence 1354, Appl1
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39	3751	US-09-355-815-1	Sequence 119, Appl1
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41	3751	US-09-355-815-1	Sequence 10, Appl1
42	3751	US-09-355-815-1	Sequence 17, Appl1
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44	3751	US-09-355-815-1	Sequence 1, Appl1
45	3751	US-09-355-815-1	Sequence 31, Appl1
46	3751	US-09-355-815-1	Sequence 45, Appl1

QY	182	TGGTGGCAAGTGGAGATGCTGACATGAAGGACATTCTCGGCCAAGTGCCTGCTGT	241	CCCCTGGCATGCAAGGACCCATCTCCAGACAGTCACATCTCTGCTTCAGTCCTGT	QY
Db	421	CCCCCTGGCATGCAAGGACCCATCTCCAGACAGTCACATCTCTGCTTCAGTCCTGT	480		1501 ACTTCAGCAGGTGGAGCTGAGCCAGASGCCAGGCCAGGGCTGGCCCAAGGCCAGGGGA
Db	242	CCCCGGCATGCAAGGACCCATCTCCAGACAGTCACATCTCTGCTTCAGTCCTGT	301		1561 GCCCCACCGCATCTCCAGACAGTCACATCTCTGCTTCAGTCCTGT
QY	481	CAGATTCACTGGCGCCGACACAGCAGTTGGAGACATCTGAGGGATGGGGCTCTGT	540		1562 GCCCCACCGCATCTCCAGACAGTCACATCTCTGCTTCAGTCCTGT
Db	302	CAGATTCACTGGCGCCGACACAGCAGTTGGAGACATCTGAGGGATGGGGCTCTGT	361		1582 GCCCCACCGCATCTCCAGACAGTCACATCTCTGCTTCAGTCCTGT
QY	541	GCCCCAGGGAGTGGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	600		1621 TGCCCTCATCTCTGGGGCTCTGGATGGGGATGGGGATGGGGATGGGGATGGGG
Db	362	GCCCCAGGGAGTGGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	421		1622 ACCGCTCTGGTCACTGGCTGCGTTACCTGGGGATGGGGATGGGGATGGGG
QY	601	TCCACCTGGCTCTGGACGGACCCAGGGAGGGATGCCGGATGGGGATGGGG	660		1681 TGTGGAAAGGAGGAGCTGACGCTTCAGCTCTGGGGACACTATCTCATACA
Db	422	TGACCTCTGGCTCTGGCTGACCCAGGGAGGGATGCCGGATGGGG	481		1502 TGTGGAAAGGAGGAGCTGACGCTTCAGCTCTGGGGACACTATCTCATACA
QY	661	TCCCCGGAGCTACCGGGCTGGTTACCTGGGGATGGGGCTCTGGATGGGG	720		1741 ACCGCGCAGTCCTTGAGACCCACCCGGTACGGGAGCTGGCTCTGGAGG
Db	482	TCCCCGGAGCTACCGGGCTGGTTACCTGGGGATGGGGATGGGGATGGGG	541		1562 ACCGCGCAGTCCTAGAGACCCGGTACGGGAGCTGGCTCTGGAGG
QY	721	ACCGCTGGTCAAGGAGTCTCAGTACCTGGGGATGGGGATGGGGATGGGG	780		1801 CCCACTCCGCTCCCTGTCCTCAATGGCTTGCTGCTCCCAATCAGCTTAC
Db	542	ACCGCTGGTCAAGGAGTCTCAGTACCTGGGGATGGGGATGGGGATGGGG	601		1562 ACCGCGCAGTCCTAGAGACCCGGTACGGGAGCTGGCTCTGGGGATTCGC
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Db	602	ACCTTGGCCCCCATGGTGGCCAGCTGGTGGCTTACCCCCGGCTGACGGTCA	661		1681 1622 ACCGCGCAGTCCTAGAGACCCGGTACGGGAGCTGGCTCTGGGGATTCGC
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Db	662	TGAGTGTGTGTCTGGGGTAGACCTCTGGGGCTCTGGGGTAGACCTCTG	721		1742 GGGCAAACCCACACCCAGGCTACAGTGGGGACTTATGGAGCTGAGAAC
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Db	722	ACACCGCCCTTGGGGAGAGACATGATTAACTGGGGCTACTCTCACGATCA	781		1801 1981 GGCAGCCGCTCTGGGGCCAGTGGGGCTGACCTCTCACGATCA
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QY	1021	GTGTGTGTGGGGCTGGTAGACTCTGGGGCTGGGGCTGGGGCTGGGG	1080		1922 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
Db	842	GTGTGTGTGGGGCTGGTAGACTCTGGGGCTGGGGCTGGGGCTGGGG	901		2101 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
QY	1081	ACTATGGGGATGGGAAACACAGCTCTCAGTCTCTGGGGATGGGGTTGAGT	1140		1922 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
Db	902	ACTATGGGGATGGGAAACACAGCTCTCAGTCTCTGGGGATGGGGTTGAGT	961		2161 AGAGCTGGAGGGCCAGTTGGGGAGGTGACCTGTGAGTCAGCTGCTCAAG
QY	1141	TTCACGGCTGTAGGGCTTCCAGGGCTACGGCTACTGACAACTGACACCTGG	1200		2162 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
Db	962	TTCACGGCTGTAGGGCTTCCAGGGCTACGGCTACTGACAACTGACACCTGG	1021		1880 2161 AGAGCTGGAGGGCCAGTTGGGGAGGTGACCTGTGAGTCAGCTGCTCAAG
QY	1201	GAGCCCTCTGCTGTGGGGGGGAATGTCCTGGGGCTGGGGCTGGGG	1260		2162 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
Db	1022	GAGCCCTCTGCTGTGGGGGGGAATGTCCTGGGGCTGGGGCTGGGG	1081		1980 2162 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
QY	1261	AGGGGAGGCCATGCCAACACTGGGGCAACCTGGGGACCCAGACCCGGCTG	1320		2162 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
Db	1082	AGGGGAGGCCATGCCAACACTGGGGCAACCTGGGGACCCAGACCCGGCTG	1141		2162 GGGAGTCGGGAGGGCCCCCAGTGGGGCTGAGTGTGAGTCAGCTGCTCAAG
QY	1321	TCTCTGGCCCTGGGGGGTGTGGCTCTGGGGCTGGGGCTGGGGCTGGGG	1380		2221 ATCTGGTCACTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG
Db	1142	TCTCTGGCCCTGGGGGGTGTGGCTCTGGGGCTGGGGCTGGGGCTGGGG	1201		2042 ATCTGGTCACTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG
QY	1381	GGCCCTGGTACTCTCAGCAATCTCTGGGGCTGGGGCTGGGGCTGGGG	1440		2281 TCAAGATCTACGCCATGCCACGGCTGGGGCTGGGGCTGGGGCTGGGG
Db	1202	GGCCCTGGTACTCTCAGCAATCTCTGGGGCTGGGGCTGGGGCTGGGG	140		2102 TCAAGATCTACGCCATGCCACGGCTGGGGCTGGGGCTGGGGCTGGGG
QY	2401	TGGCGTGTGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	2460		2341 ATTCTCTGAAAGGGTGAAGATGTCAGTCAGTCAGTCAGTCAGTCAGTC
Db	2204	TGGCGTGTGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	2263		2144 ATTCTCTGAAAGGGTGAAGATGTCAGTCAGTCAGTCAGTCAGTCAGTC
QY	2461	ACCTCAACCGAGTCCTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	2400		2264 ACCTCAACCGAGTCCTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG
Db	2324	GGAGGGCCAGTCCTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	2383		2521 GGAGGGCCAGTCCTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG

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Db 2504 GCGGAACCTCATGCGGGACTATTAACCGTGAGGGGGAGTGCAGCCATCC 2563
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Db 2564 GCTGGANGGCCGGAGTGCACCTCATGGGAGTGCAGCCATCC 2623
QY 2821 CCTTGGTGTGACCCCTGGGAGACTTCACGTTGCGAGGCTGGAGC 2880
Db 2624 CCTTGGTGTGACCCCTGGGAGACTTCACGTTGCGAGGCTGGAGC 2683
QY 2881 TACCGGAGGAGGAGGATCTGAGAACGGGGAGTTTCCGGGACAGGGCGAGG 2940
Db 2684 TCACCGGAGGAGGAGGATCTGAGAACGGGGAGTTTCCGGGACAGGGCGAGG 2743
QY 2941 TGTACTCTGTCGCCGGGCCCTGCCCTGCCGAGGGCTATATGAGCTGAGCTGGGT 3000
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QY 3001 GGAGCGGGAGCTGAGCCAGGACACCCCTTCCAGCTGACATCGTTGCGAGG 3060
Db 2804 GGAGCGGGAGCTGAGCCAGGACACCCCTTCCAGCTGACATCGTTGCGAGG 2863
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Db 2864 ATGCACTCACACGGGTTGAACTACATCCAGCTGAGCTGCCCTCCAGCTGAGG 2923
QY 3121 GGGAAAGCCACTGACACTAAACAAGGGACATAAGGCTGAGCTGGAGCTGGGG 3179
Db 2924 GGGAAAGCCACTGACACTAAACAAGGGACATAAGGCTGAGCTGGGG 2983
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Db 3040 GCTGAGGCCCTTCCGCCCTTCCGGACACTCATGAGCTGCCCTTCCGGTTCTTC 3099
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Db 3100 CTAGAGGCCCTGCGCCACCCAGCTGGCTCTGGAGGGATCTCCACCCCTTC 3159
QY 3360 TAGCATCCTGGGAAGGGGGAGAATAATAGGATAGACACTGGCATGGCCATT 3419
Db 3160 TASCATCCTGGGAAGGGGGAGAATAATAGGATAGACACTGGCATGGCCATT 3219
QY 3420 GGACCACTGGGCCACACTGGACACACTGATCTGGAGGCGCG-CGCCAGT 3478
Db 3220 GGACCACTGGGCCACACTGGACACACTGATCTGGAGGCGCG-CGCCAGT 3279
QY 3479 TCTCTCTCTGACACTGGACCCCTCTGGCTGAGATCGGGGGAGGAGCA 3538
Db 3280 TCTCTCTCTGACACTGGACCCCTCTGGCTGAGATCGGGGGAGGAGCA 3339
QY 3339 GAAGGAGGAAATGTTCTTCTGCTGCTGTACTGCTCTACTTGGCTGCTT 3598
Db 3340 GAAGGAGGAAATGTTCTTCTGCTGCTGTACTGCTCTACTTGGCTGCTT 3399
QY 3599 TCTCTCTCTGACACTGGACACTGGACCTGGGGTAGGCCGCCAGCCCTAGCA 3657
Db 3400 TCTCTCTCTGACACTGGACACTGGACCTGGGGTAGGCCGCCAGCCCTAGCA 3459
QY 3658 CCCCACTTCCACTTGGCTCTGTAGCTAGACTCTCTAAGCTATACGTTCTG 3717

RESULT 2
; Sequence 4549, Application US/10060036
; Publication No. US200300731441
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Repler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121 566
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4549
; LENGTH: 3849
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-060-036-4549

Query Match 91.2%; Score 3613.4; DB 9; Length 3849;
Best Local Similarity 95.9%; Pred. No. 0; Mismatches 31; Indels 130; Gaps 3;
Matches 3792; Conservative 0;

QY 2	GGGCGAGACTGGGGTACGGGCTTAAGAGATCTGGCTGGAGGGCCCCACAGC 61
Db 24	GGCCCTGGAGGGAGCTGAGCCAGGGCCCTGGGGCCACCTTGAGGGCCAGC 83
QY 62	TGCTTGCGGAGCCCTCCGGACCCGGCCGGCCACCTTGAGGGCCAGC 121
Db 84	TGCTTGCGGAGCCCTCCGGACCCGGCCGGCCACCTTGAGGGCCAGC 143
QY 122	GGCTCTGGAGCCCTCCGGACCCGGCCGGCCACCTTGAGGGCCAGC 181
Db 144	GGCCCTGGCTCCCGCCCTCCGGACCCGGCCAGC 203
QY 182	CCTGGAGGGCCGGGGAGGGAGGGAGGGCTGAGGGCTCTGAGGGGGCTT 241
Db 204	CGGGCTGGAGCCCTGGGGAGGGAGGGCTGAGGGCTCTGAGGGGGCTT 263
QY 242	CACCTGGATGGGGTGGACTGGAGGATGCGAGAGATGCGAGGGCTGCTG 301
Db 264	CACCTGGATGGGGTGGACTGGAGGATGCGAGAGATGCGAGGGCTGCTG 323
QY 302	GCCCGGGATCAGGGATGGGGAGGGGGCTGCTGAGGGCTGCTGCTG 361
Db 324	GCCCGGGATCAGGGATGGGGAGGGGGCTGCTGCTGCTGCTGCTG 383
QY 362	GGTGGCAAGTGGAGATGCTGACAGCTGAGGGACATTTGATCCGCACTG 421

QY 2582 CCAGATCGCTCCGGCATGGCATGGCTACACTTGTACATGGACCTGGC 2641
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 Db 2475 CCAGATCGCTCCGGCATGGCTACACTGGCACACTCAACTTGACATCGGACTGGC 2534
 QY 2642 CACGGGAACACTGCTTAGTGGGAAATTACACATCAAAATCGAGACTTGGATGAG 2701
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 QY 2762 CTGGATGGCCTGGGAGTCAGCTGGGAAATTACACATCAAAATCGAGACTTGGATGAG 2821
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 Db 2775 CACCGACGGAGCGTCATCGAGAACGCGGGACTCTCGGGACAGGGCGCAGGT 2834
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 QY 3002 GACGGGGAGTCAGACGACGGGACACCCCTTCACAGCTGATCGGTCTGGGAGGA 3061
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 Db 2895 GACGGGGAGTCAGACGACGGGACACCCCTTCACAGCTGATCGGTCTGGGAGGA 2954
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 QY 3062 TGCACCTCACACGGTGTGAAATCACACATCACACATCACACATCACACATCACAC 3121
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 Db 2855 TGACTCACACACGGTGTGAAATCACACATCACACATCACACATCACACATCACAC 3014
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 Db 3015 GGAGCCAGTGTGACACTAAACAGAGGACACAACTGCACTCTGCCCTGCCGAC 3074
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 Db 3075 AGCCATCACCTAATAGAGGGAGTGAGACTGAGGAGGCTGGCCACCCAGGGAGC 3134
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 QY 3242 TGTGCCCCCTCCCGCTTCCGAGAACACTCTCATGAGCCCTCTGTCTCTCT 3301
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 Db 3135 TGTGCCCCCTCCCGCTTCCGAGAACACTCTCATGAGCCCTCTGTCTCTCT 3194
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 QY 3302 AGAAGCCTGAGCCACCCAGCTGGCTCTGGGGATCTCCACCCCTCTCA 3361.
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3195 AGAAGCCTGAGCCACCCAGCTGGCTCTGGGGATCTCCACCCCTCTCA 3254
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3362 GGCATCTCTGGGAAGGGTGGGGAGAATAATAGGATAGACACGACATGGACATGGCTCT 3421.
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3255 GGCATCTCTGGGAAGGGTGGGGAGAATAATAGGATAGACACGACATGGCTCT 3314
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3422 AGCAGCTGGGCCCATGGACACACAGATCCTGAGAGGGCTGGCTCT 3480.
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3315 AGCAGCTGGGCCCATGGACACACAGATCCTGAGAGGGCTGGCTCT 3374
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3481 TCTCTCCTGTCACACACTGGACCCACTGGCTGAGAATCTGGGGAGGACAGA 3540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3375 TCTCTCCTGTCACACACTGGACCCACTGGCTGAGAATCTGGGGAGGACAGA 3434
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3541 AGGAGGAAATGTCTCTGGCTGAGACATGGCTCT 3600
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3435 AGGAGGAAATGTCTCTGGCTGAGACATGGCTCT 3494
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3601 CTCTCTCATCACCTGAAACACTGGACCTGGGGATGCCACCCCTGTCACCC 3660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3495 CTCTCTCATCACCTGAAACACTGGACCTGGGGATGCCACCCCTGTCACCC 3554
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db	17	GTTGGAATCTGGAAAGTGTGCCAAGAGATGCTGCCAACCCCAATTGGCGAGGGATCG	76	Qy
Qy	316	GAGCTTGGAACAGGGCCCTGTCTACTGTCGCTCTGGCAAGTGAG	375	Qy
Db	77	GAGCTTGGAACAGGGCCCTGTCTACTGTCGCTCTGGCAAGTGAG	136	Db
Db	376	ATGCAGACATGAGGGACATTTGATCCTGCAAGTGGCGCATGG	435	Qy
Qy	436	ACCGGACATCCAGAGGACATTGATCCTGCAAGTGGCGCATGG	495	Qy
Db	197	ACCGGACATCCAGAGGACATTGATCCTGCAAGTGGCGCATGG	256	Db
Qy	496	CCGGCACAGGAGTTGAGACGGACGGGATGGGCTGGTGGCGAGG	555	Qy
Db	257	CCGGCACAGGAGTTGAGACGGACGGGATGGGCTGGTGGCGAGG	316	Db
Db	556	TGTTGCCAGAGGGAGGAGTACTCAGGGATACACGACTCCACCG	615	Qy
Db	317	TGTTGCCAGAGGGAGGAGTACTCAGGGATACACGACTCCACCG	376	Qy
Qy	616	TGGTGGCACCCAGGGACGGATGGGGCTGGCAAGGAGTCTCGGAG	675	Qy
Db	377	TGGTGGCACCCAGGGACGGATGGGGCTGGCAAGGAGTCTCGGAG	436	Db
Qy	676	GGCTCGTACTCCGGGATGTCGGCGTGGATGGCTGGAGGACCG	735	Qy
Db	437	GGCTCGTACTCCGGGATGTCGGCGTGGATGGCTGGAGGACCG	496	Db
Db	736	AGGACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	795	Qy
Qy	497	AGGACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	556	Qy
Db	796	TGTTGCCACTTGGCTCACCCGGGCGACCGGGTCAAGAGTCTCG	855	Qy
Db	557	TGTTGCCACTTGGCTCACCCGGGCGACCGGGTCAAGAGTCTCG	616	Db
Qy	856	GGTAGAGCTATGGCTCTGGAGGATGACTCTGCTTAACCCCC	915.	Qy
Db	617	GGTAGAGCTATGGCTCTGGAGGATGACTCTGCTTAACCCCC	676	Db
Db	916	GGCAGACATGATTTATCTGGGGGTGACCTAACGACTCCACCT	975	Qy
Qy	677	GGCAGACATGATTTATCTGGGGGTGACCTAACGACTCCACCT	736	Qy
Db	976	CCGGCGACTCGAGTATGGGCTTGGCCACCTGGGAGATGGTG	1035	Qy
Db	737	CCGGCGACTCGAGTATGGGCTTGGCCACCTGGGAGATGGTG	796	Db
Qy	1036	ATGACTTGGAAAGTCAGGAGCTGGGCTCTGGCAGGATGACTAT	1095	Qy
Db	797	ATGACTTGGAAAGTCAGGAGCTGGGCTCTGGCAGGATGACTAT	856	Db
Db	1096	GCAACACAGCTTCAGGGCTGGGAGATGAGTGGAGTGGAGG	1155	Qy
Qy	857	GCAACACAGCTTCAGGGCTGGGAGATGAGTGGAGG	916	Qy
Db	1156	CCTTCCAGCTTGAGGACACGTTGAGTGGAGTGGAGG	1215	Db
Qy	917	CCTTCCAGCTTGAGGACACGTTGAGTGGAGG	976	Db
Qy	2116	GGCCCCAGAGTGGATTCCTGATCGACTCGCTCGAGGAGCTTG	2175	Qy
Db	1877	GGCCCCAGAGTGGATTCCTGATCGACTCGCTCGAGGAGCTTG	1936	Db
Db	2176	GGAGTTGGGGAGGTGCACTTGTTGAGTGGAGTGGAGG	2235	Qy
Qy	1937	GCGAGTGGGGAGGTGCACTTGTTGAGTGGAGTGGAGG	1996	Qy
Db	2236	ATTTCCCTTAATGTCGATAAGGACACCTTGCTGGTAGCTCAAG	2295	Db
Qy	1997	ATTTCCCTTAATGTCGATAAGGACACCTTGCTGGTAGCTCAAG	2056	Qy
Db	2296	CGATGCCACAGAATGCCGCTCTCTTCTCCAGGATGATTCGAA	2355	Db
Db	2057	CGATGCCACAGAATGCCGCTCTCTTCTCCAGGATGATTCGAA	2098	Db
Qy	2356	TGAGATCTGTGAGGCTCAAGGACCCACATCATGGAGGGACCT	2415	Qy
Db	2099	TGAGATCTGTGAGGCTCAAGGACCCACATCATGGAGGGACCT	2158	Db
Qy	2416	AGGAGACCCCTGGCTGAGTACTGACTCATGGAGGGACCTAAC	2475	Qy
Db	2159	AGGAGACCCCTGGCTGAGTACTGACTCATGGAGGGACCTAAC	2218	Db

QY	2476 TCACTGCCAACCGAGCTGGAGGACAGGACGCCAGGGAGGGGGCCCTGGGAGGGGGCAGGGCTGGT 2535	Db	3555 TTTCTCTTGCTGCTGCTGTGCTGTTGCTGCTGGCTCTTCCTCCCATCACCT 3614
Db	2219 TCACTGCCAACCGAGCTGGAGGACAGGACGCCAGGGAGGGGGCCCTGGGAGGGGGCAGGGCTGGT 2278	Db	3213 TTCTCTTGCTGCTGCTGTGCTGCTGCTGGCTCTTCCTCCCATCACCT 3272
QY	2536 CGCAGGGGCCAACCATCATGACTACCCAAATCTGCICATGGCCAGCCAGATGCTCC 2595	Db	3615 GAAACATGGGCCCTGGGGTAACCCCCCCCAGCCCTCAGTCACCCCACTTCCACTG 3674
Db	2279 CGCAGGGGCCAACCATCATGACTACCCAAATCTGCICATGGCCAGCCAGATGCTCC 2338	Db	3273 GAAACATGGGCCCTGGGGTAACCCCCCCCAGCCCTCAGTCACCCCACTTCCACTG 3332
QY	2596 GCTTGCGTATCCTGGCCACACTCACTCACTGTCATGGGACTGGCCACCGGAACATGCC 2655	Db	3675 CAGCTGTAGCTAGACTCTCTAAGCTTACGGTTCAGTCAGTCAGTCAGGGACTGGCTCC 3734
Db	2339 GCTTGCGTATCCTGGCCACACTCACTCACTGTCATGGGACTGGCCACCGGAACATGCC 2398	Db	3333 CAGCTGTAGCTAGACTCTCTAAGCTTACGGTTCAGTCAGTCAGTCAGGGACTGGCTCC 3392
QY	2656 TAGTGGAAATTTCACCATCAAATGCGAGACTTGGCATGAGCCGACCTCTATG 2715	Db	3735 GGGGGAAAGGGGACACGCCCATAGCCCTGGGGTGCACATCTACTGAGCTGC 3794
Db	2399 TAGTGGAAATTTCACCATCAAATGCGAGACTTGGCATGAGCCGACCTCTATG 2458	Db	3393 GGGGGAAAGGGGACACGCCCATAGCCCTGGGGTGCACATCTACTGAGCTGC 3452
QY	2716 CTCGGGACTATACCGTGTGAGGGCCGGACTCTGTCGCTGCGCATGGCCGAACTCTATG 2775	Db	3795 CACATGATTTCTTAATACTCTGGGTTGTCATTTGGGGAGGACAGAGAT 3854
Db	2459 CTCGGGACTATACCGTGTGAGGGCCGGACTCTGTCGCTGCGCATGGCCGAACTCTATG 2518	Db	3453 CACATGATTTCTTAATACTCTGGGTTGTCGCTGCGCATGGCCGAACTCTATG 3512
QY	2776 AGTGCACCTCTATGGGGAGGTACGACTGGGAGTGAAGCTGGTGTGGCCCTTGIGTACCC 2835	Db	3855 TTTCAGATTAATATGGACCTAGCTTGAGGCAATTAACTCCCTGGGCTTGIGTACCC 3914
Db	2519 AGTGCACCTCTATGGGGAGGTACGACTGGGAGTGAAGCTGGTGTGGCCCTTGIGTACCC 2978	Db	3513 TTTCAGATTAATATGGACCTAGCTTGAGGCAATTAACTCCCTGGGCTTGIGTACCC 3572
QY	2836 TCTGGGAGGTCTGATGCTCTGTTAGGGCCAGCCCTGGGAGCTCACCAGGAGCAGG 2895	Db	3915 ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAA 3953
Db	2579 TCTGGGAGGTCTGATGCTCTGTTAGGGCCAGCCCTGGGAGCTCACCAGGAGCAGG 2638	Db	3573 ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAA 3611
QY	2896 TCATCGAGAACGGGGAGGTCTTCCGGGACAGGGCCAGGGCGACCTCAGGAGCAGG 2895	Db	
Db	2639 TCATCGAGAACGGGGAGGTCTTCCGGGACAGGGCCAGGGCGACCTCAGGAGCAGG 2698	Db	
QY	2956 CGCCTCTCTGCGCGGGCCPATATAGGCTGATCCTGGGCTTGGGAGGAGGCTG 3015	Db	
Db	2699 CGCCTCTCTGCGCGGGCCPATATAGGCTGATCCTGGGAGGAGGAGGCTG 2758	Db	
QY	3016 AGCAGGACACCCCTTCCAGCTGATCGGTCCTGGCAGAGGATGACTCACAGG 3075	Db	
Db	2759 AGCAGGACACCCCTTCCAGCTGATCGGTCCTGGCAGAGGATGACTCACAGG 2818	Db	
QY	3076 TGTGAATCACATCCAGCTGCGCCCTCTCAGGAGTATGACTGTCGGGCTG 3135	Db	
Db	2819 TGTGAATCACATCCAGCTGCGCCCTCTCAGGAGTATGACTGTCGGGCTG 2878	Db	
QY	3136 CTAACACAAGGACCAATGCACTCTGGCCCTCCAGGGAGCTGATGCCATCCCT 3195	Db	
Db	2879 CTAACACAAGGACCAATGCACTCTGGCCCTCCAGGGAGCTGATGCCATCCCT 2938	Db	
QY	3196 ATAGGGCAGTGAGCTGAGGTGGACTGGGCCACCCAGGGAGCTGATGCCCTC 3255	Db	
Db	2939 AATAGGGCAGTGAGCTG----- 2958	Db	
QY	3256 CCCTTCCTGGACACACTCTCAGTCGCTCCTCTGTCCTCCCTCTAGAAGGCCCTG 3315	Db	
Db	2959 -----AGAAGGCCCTGCG 2972	Db	
QY	3316 CCCACCCAGCTGGTCTCTGGATGCCATCTCCACCCCTCTGGCATGCCACCTGG 3375	Db	
Db	2973 OCACACCACTGGATGCCATCTGGCATGCCACCTGGCATGCCACCTGG 3032	Db	
QY	3376 AAGGGGGAGAATATGGATAGCACTGGACATGGGACATGGGACCTGGGCC 3435	Db	
Db	3033 AAGGGGGAGAATATGGATAGCACTGGACATGGGACATGGGACCTGGGCC 3092	Db	
QY	3436 ACTGGGACAAACTGATCTCTGGAGAGGTGGCTGCG-CCCCAAGCTCTCTCCTCCT 3494	Db	
Db	3093 ACTGGGACAAACTGATCTCTGGAGAGGTGGCTGCG-CCCCAAGCTCTCTCCTCCT 3494	Db	
QY	3495 ACATGGGACAAACTGATCTCTGGAGAGGTGGCTGCG-CCCCAAGCTCTCTCCTCCT 3554	Db	
Db	3153 ACATGGGACAAACTGATCTCTGGAGAGGTGGCTGCG-CCCCAAGCTCTCTCCTCCT 3212	Db	
QY	3555 TTTCTCTTGCTGCTGCTGTGCTGCTGGCTCTTCCTCCCATCACCT 3614	Db	
Db	3213 TTCTCTTGCTGCTGCTGTGCTGCTGGCTCTTCCTCCCATCACCT 3272	Db	
QY	3615 GAAACATGGGCCCTGGGGTAACCCCCCCCAGCCCTCAGTCACCCCACTTCCACTG 3674	Db	
Db	3273 GAAACATGGGCCCTGGGGTAACCCCCCCCAGCCCTCAGTCACCCCACTTCCACTG 3332	Db	
QY	3675 CAGCTGTAGCTAGACTCTCTAAGCTTACGGTTCAGTCAGTCAGGGACTGGCTCC 3734	Db	
Db	3333 CAGCTGTAGCTAGACTCTCTAAGCTTACGGTTCAGTCAGTCAGGGACTGGCTCC 3392	Db	
QY	3735 GGGGGAAAGGGGACACGCCCATAGCCCTGGGGTGCACATCTACTGAGCTGC 3794	Db	
Db	3393 GGGGGAAAGGGGACACGCCCATAGCCCTGGGGTGCACATCTACTGAGCTGC 3452	Db	
QY	3795 CACATGATTTCTTAATACTCTGGGTTGTCATTTGGGGAGGACAGAGAT 3854	Db	
Db	3453 CACATGATTTCTTAATACTCTGGGTTGTCGCTGCGCATGGCTG 3512	Db	
QY	3855 TTTCAGATTAATATGGACCTAGCTTGAGGCAATTAACTCCCTGGGCTTGIGTACCC 3914	Db	
Db	3513 TTTCAGATTAATATGGACCTAGCTTGAGGCAATTAACTCCCTGGGCTTGIGTACCC 3572	Db	
QY	3915 ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAA 3953	Db	
Db	3573 ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAA 3611	Db	

Db	181	TGGCCGACAACTAAGGGCACCTGGGACCCAGAGGCCGACTGTGTCAGTGCCC	240	QY	2413	TGCAGGACCCCCCTGTGATGATACTGACTAATGAGAACGGGACCTCACCAGT	2472
QY	1333	TGGCCGCGGTGGCTTCGCAAGTGGCGCTTCCTCGAGTGGCGCTTCCTCGAGT	1392	Db	1303	TGCAGGACACCCCCCTGTGATGATACTGACTAATGAGAACGGGACCTCACCAGT	1362
Db	241	TGGCCGCGGTGGCTTCGCAAGTGGCGCTTCCTCGAGTGGCGCTTCCTCGAGT	300	QY	2473	TCTTAGTGGCCACAGCTGGAGGCAAGCAGGGAGGGGCCCTGGGACCGCCTAACCGT	2532
QY	1393	TCTCAGGGAATCTCTCATCTGATGATGTAACAAATTCCTCTGGACTGGAG	1452	Db	1363	TCTTAGTGGCCACAGCTGGAGGCAAGCAGGGAGGGGCCCTGGGACCGCAGG	1422
Db	301	TCTCAGGGAATCTCTCATCTGATGATGTAACAAATTCCTCTGGACTGGAG	360	QY	2533	CTGCAGGGGCCACATGCTACCTGGAGGAGGGAGGGGCCCTGGGACCGCAGG	2592
QY	1453	GCACCTTCGCCACGCCCTGGTGCCCTGGCCAACTCCACACTTCAGAGT	1512	Db	1423	CTGCAGGGGCCACATGCTACCTGGAGGAGGGAGGGGCCCTGGGACCGCAGG	1482
Db	361	GCACCTTCGCCACGCCCTGGTGCCCTGGCCACCTCCACACTTCAGAGT	420	QY	2593	CGGGATGCGCTATGGCACACTCACTTGTACATGGACCTGGCACCGGAACT	2652
QY	1513	TGGAGCTGGAGCCAGAGGCCAGGCCAGGGAGGGGCCAGGCCA	1572	Db	1483	CGGGATGCGCTATGGCACACTCACTTGTACATGGACCTGGCACCGGAACT	1542
Db	421	TGGAGCTGGAGCCAGAGGCCAGGCCAGGGAGGGGCCAGGCCA	480	QY	2653	GCCTAGTTGGGAATTTCACCACTACCGCTGTGCTGCTGCTGCTGCTGCT	2712
QY	1573	TCTCTAGGAGGCTGGTGCCATCATCGCTGCTGCTGCTGCTGCTGCT	1632	Db	1543	GCCTAGTTGGGAATTTCACCACTACCGCTGTGCTGCTGCTGCTGCTGCT	1602
Db	481	TCTCTAGGAGGCTGGTGCCATCATCGCTGCTGCTGCTGCTGCTGCT	540	QY	2713	ATGGGGGACTATTACGGTGTGCGGGGGGGCGTGCGGCCATCGCTGATGGCT	2772
QY	1633	TCTCTAGGAGGCTGGTGCCATCATCGCTGCTGCTGCTGCTGCTGCT	1692	Db	1603	ATGCTGGGACTATTACGGTGTGCGGGGGGGCGTGCGGCCATCGCTGATGGCT	1682
Db	541	TCTGGGGCTACAGTGCGAGGYCTCAGCAAGGTYAACGGGGGTTGGAGAGC	600	QY	2773	GGGATGCACTCATGGGAAGTTACGACTGCGAGTGGAGTGGGCTTGGTGTG	2832
QY	1693	AGCTGAGGTTACCTCTCTCTGGAGGAACTATTCATCACACGCCAGTC	1752	Db	1663	GGGATGCACTCATGGGAAGTTACGACTGCGAGTGGAGTGGGCTTGGTGTG	1722
Db	601	AGCTGAGGTTACCTCTCTCTGGAGGAACTATTCATCACACGCCAGTC	660	QY	2833	CCCTTGGGGAGTTGATGCTCTCTAGGGCCACCCCTTGGGAGCTCACCRGASC	2892
QY	1753	CTAGAGAGCCACCCGTAACAGAGGCCCGGCTGTGAGTACCGCCACCCGTC	1812	Db	1723	CCCTTGGGGAGTTGATGCTCTCTAGGGCCACCCCTTGGGAGCTCACCRGASC	1782
Db	661	CTAGAGAGCCACCCGTAACAGAGGCCCGGCTGTGAGTACCGCCACCTYGT	720	QY	2893	AGGTATGAGAACGGGGAGTCTCGGGGACTTCGAGGAGCCAGGGCCAGGG	2952
QY	1813	CCTGAGTCCCAATGCTCTGGTGTCTCTCTCAATCAGCTTACCCCTCTCG	1872	Db	1783	AGGTATGAGAACGGGGAGTCTCGGGGACTTCGAGGAGCCAGGGCCAGGG	1842
Db	721	CCTGAGTCCCAATGCTCTGGTGTCTCTCTCAATCAGCTTACCCCTCTCG	780	QY	2953	GGCCCTGCTGCCGAGGGCTATAGCTGCTGCTGGGCTTGGGAGT	3012
QY	1873	CCACTTACGCCGCTGCCCTCGAGGCCCGCCGCCACCCGCAACCCA	1932	Db	1843	GGCCCTGCTGCCGAGGCTGCTGCCCA-GGCYVATATGAGCTGATGCTCG	1901
Db	781	CCACTTACGCCGCTGCCCTCGAGGCCCGCCGCCACCCGCAACCCA	840	QY	3013	CTGAGCAGCACACCCCTTCCAGCTGATCGATCGCTCCGGCTGGAGCTCACCA	3072
QY	1933	CCAAACCCAGGCTTACAGGGGACTATAGGACCTAATAGGACCTAAGG	1992	Db	1902	CTGAGCAGCACACCCCTTCCAGCTGATCGATCGCTCCGGCTGGAGGATGCACT	1961
Db	841	CCAAACCCAGGCTTACAGGGGACTATAGGACCTAATAGGACCTAAGG	900	QY	3073	CGGTGAACTCACATCCAGCTGCCCTCCCTGGGAGTGATCGAGGAACTCAGT	3132
QY	1993	TGCCCCACCTCCCAAGAACGGTGTGCTGAGGAGGACATGTGTTACCTTC	2052	Db	1962	CGGTGAACTCACATCCAGCTGCCCTCCCTGGGAGTGATCGAGGAACTCAGT	2021
Db	901	TGCCCCACCTCCCAAGAACGGTGTGCTGAGGAGGACATGTGTTACCTTC	960	QY	3133	ACACTAACAGGAGCACATGGCACCTCTGCCCTCCCTCCAGAACGCCAAC	3192
QY	2053	AGGCGTCACGGGGCACACCTATGCTGCTGCACTGCCCCAGGGCACTCGGG	2112	Db	2022	ACACTAACAGGAGCACACCAATGCACTGCCCTCTGCCCTCCAGGCCAAC	2081
Db	961	AGGCGTCACGGGGCACACCTATGCTGCTGCACTGCCCCAGGGCACTCGGG	1020	QY	3193	TCTAATAGGGCAGTGGAGACTGCGAGTGGGGCTGGGCCACCCAGGAGCTG	3252
QY	2113	ATGGGGCCCGAGGAGTGGGGCTGGCTGAGCTGCTGCTGCTGCTGCT	2172	Db	2082	TCTAATAGGGCAGTGGAGACTGCGAGTGGGGCTGGGCCACCCAGGAGCTG	2141
Db	1021	ATGGGGCCCGAGGAGTGGGGCTGGCTGAGCTGCTGCTGCTGCTGCT	1080	QY	3253	CTCCCTCTGGAGACACTCTGAGTGGGGCTGGGCCACCCAGGAGCTG	3312
QY	2173	AGGGCAGTGGGGAGGGCACCTGGAGGAGCTGCTGCTGCTGCTGCT	2232	Db	2142	CTCCCTCTGGAGACACTCTGAGTGGGGCTGGGCCACCCAGGAGCTG	2201
Db	1081	AGGGCAGTGGGGAGGGCACCTGGAGGAGCTGCTGCTGCTGCTGCT	1140	QY	3313	TGCCACCCAGCTGGATCCCTCCACCTCTAGCCATCCCTG	3372
QY	2233	TGATTCCTTAATGGGGTGTAGGGCACCTTGTGGTGTGCTGAGCTTC	2292	Db	2202	TGCCACCCAGCTGGATCCCTCCACCTCTAGCCATCCCTG	2261
Db	1141	TGATTCCTTAATGGGGTGTAGGGCACCTTGTGGTGTGCTGAGCTTC	1200	QY	3373	GGGAGGGGGAGGAAATAGGGTAGACACTGGACATGGCCCATGGACCTGG	3432
QY	2293	GCGCAGATGCAAGAGGCCAACATCTGCTGCTGCTGCTGCT	2352	Db	2262	GGGAGGGGGAGGAAATAGGGTAGACACTGGACATGGCCCATGGACCTGG	2321
Db	1201	GGCGCAGATGCAAGAGGCCAACATCTGCTGCTGCTGCTGCT	1242	QY	3433	CCCACTGGAGACACTGATGGGGGGCTGGGCCACCCAGGAGCTG	3491
QY	2353	AGGTAGAGATGAGGAGCTCAAGGACCCAACTCATCTGCTGCTGCT	2412	Db	2322	CCACTGGAGACACTGATGGGGGGCTGGGCCACCCAGGAGCTG	2381
Db	1243	AGGTAGAGATGAGGAGCTCAAGGACCCAACTCATCTGCTGCTGCT	1302				

QY 3492 CACACACGGACCCACAGCGCTGAGAATCTGGGGTGGAGGAGCACAGAGGAGGAA 3551
 Db 2382 CACACACTGGACCCCACUGCGCTGAGAATCTGGGGTGGAGGAGCACAGAGGAGAA 2441
 QY 3552 ATGGTCCTCTGTGCGCTGCGTCACTGACTCTCCTCAGCTGCGTGGGGCTCTCTCTCCATCA 3611
 Db 2412 ATGTTCTTGTCGCTGCTCTGTACTGTCCTGACTGCTGCGTGGGCCTCTCTCCATCA 2501
 QY 3612 CCTGAAACACTGGACCTGGGGAGCCGCGCCAGCCTCAGCACCCACTCCAC 3671
 Db 2502 CCTGAACACTGGACCTGGGGAGCCGCGCCAGCCTCAGCACCCACTCCAC 2561
 QY 3672 TTGAGCTTGAGCTGACTCTCTAGCTCTAGCTTACGTTCTCTGGTAATTCG 3731
 Db 2562 TTGAGCTTGAGCTGACTCTCTAGCTTACGTTCTCTGGTAATTCG 2621
 QY 3732 ATGGGGGAAGAGGGAGCAACGGCCCATAGCTTGGGTAGCCCGCCAGCCCTCACCCACTCCAC 3791
 Db 2622 ATGGGGGAAGAGGGAGCAACGGCCCATAGCTTGGGTAGCCCGCCAGCCCTCACCCACTCCAC 2681
 QY 3792 TCCACACATGATTCTCAATACTTGGGGTGTCACTTTGGGGAGACACA 3851
 Db 2682 TGCCACATGATTCTCAATACTTGGGGTGTCACTTTGGGGAGACACA 2741
 QY 3852 GATTTTACACTATATGGACCTAGTTGAGGCAATTAACTCCCTGCACTAGGGAG 3911
 Db 2742 GATTTTACACTATATGGACCTAGTTGAGGCAATTAACTCCCTGCACTAGGGAG 2801
 QY 3912 GTATAATAAGGTGAGTTTCCACAAAAAAA 3953
 Db 2802 GAAATAATAAGGTGAGTTTCCACAAAAAAA 2843

RESULT 5
 US-09-223-490-7
 Sequence 7, Application US/09223490
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Mark, Melanie R.
 APPLICANT: Scadden, David T.
 APPLICANT: Baker, Kevin P.
 TITLE OF INVENTION: Protein Tyrosine Kinases
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/223,490
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/170,558
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,615
 REFERENCE/DOCKET NUMBER: 854C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1996
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1197 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-223-490-7

Query Match 30.1%; Score 1192.2; DB 10; Length 1197;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1194; Conservative 0; Mismatches 3; Insets 0; Gaps 0;

QY 375 GATGCTGACATGAGGGACATTTCATCCCTGGCCAGTGSCTGGCATG 434
 Db 1 GATGCTGACATGAGGGACATTTCATCCCTGGCCAGTGSCTGGCATG 60
 QY 435 GACGGACATCCAGACAGTGAATCTCGTCTCCAGTCTGTCAGATCCACTGCC 494
 Db 61 GACGGACATCCAGACAGTGAATCTCGTCTCCAGTCTGTCAGATCCACTGCC 120
 QY 495 GCCGCCACAGCAGCTGGAGGAGGTGAGGGATGGGGATGGGCCAGGGTG 554
 Db 121 GCCGCCACAGCAGCTGGAGGAGGTGAGGGATGGGGATGGGCCAGGGTG 180
 QY 555 GTGTTTCCCAGGGAGGAGTACTGAGGTGATCTCAAGCACTCCACCTGGTGT 614
 Db 181 GTGTTTCCCAGGGAGGAGGAGTACTGAGGTGATCTCAACGGACTGACCTG 240
 QY 615 CTGTTGGGACCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 674
 Db 241 CTGGTGGGACCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 300
 QY 675 CGGTGCGTACTCCGGATGGTGGCCCTGGGGCTGGGGCTGGGGCTGGGG 734
 Db 301 CGGTGCGTACTCCGGATGGTGGCCCTGGGGCTGGGGCTGGGGCTGGGG 360
 QY 735 GAGGTGATCTCAGGGCAATGGACCTGGGGAGCTGGGGCTGGGGCTGGGG 794
 Db 361 GAGGTGATCTCAGGGCAATGGACCTGGGGAGCTGGGGCTGGGGCTGGGG 420
 QY 795 ATGGTGGCGACGCTGGTGTGCTTAACCCCGGGCTGACGGGCTCATGTCCTG 854
 Db 421 ATGGTGGCGACGCTGGTGTGCTTAACCCCGGGCTGACGGGCTCATGTCCTG 480
 QY 855 CGGGTAGAGCTCTTATGGCCCTGGGGCTGGGGGGGGGGGGGGGGGGGG 914
 Db 481 CGGGTAGAGCTCTTATGGCCCTGGGGCTGGGGGGGGGGGGGGGGGGGG 540
 QY 915 GGGGAGACATGTTATCTGAGGGCGTACCTCAAGACACTACCTATGGGG 974
 Db 541 GGGGAGACATGTTATCTGAGGGCGTACCTCAAGACACTACCTATGGGG 600
 QY 975 ACCTGSGGGACTGCGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1034
 Db 601 ACCTGSGGGACTGCGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 660
 QY 1035 GATGACTTGGAGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1094
 Db 661 GATGACTTGGAGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 720
 QY 1095 AGGACACAGCTCTCAGTGGCTCTGGAGTGGGGGGGGGGGGGGGGGGGG 1154
 Db 721 AGGACACAGCTCTCAGTGGCTCTGGAGTGGGGGGGGGGGGGGGGGGGG 780
 QY 1155 GCCTCCAGGCTGCGAGTGCAGCTGCGCTGGGGGGGGGGGGGGGGGGGG 1214
 Db 781 GCCTCCAGGCTGCGAGTGCAGCTGCGCTGGGGGGGGGGGGGGGGGGGG 840
 QY 1215 GCGGGGGGGAAATGTCCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1274
 Db 841 GCGGGGGGGAAATGTCCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 900
 QY 1275 CGCCACACGAGGGGCAACCTGGGGGAGCCCCGGCGCTGCTCAGTGGCCCT 1334

Db 901 CGCCAGAACCTAGGGGCAACTGGGGACGCCAGCCCCGGGCTCGAGGCCCT 960 QY 2971 AGGCCTATATGAGCTGACTTCTGCTGCTGGAGCTGAGCAGGCCACCT 3030 Db 1335 GGCAGCTGTGGCGCTTCTGCACTGCGCTTCCTTTGGGGCCCTGGTACTC 1394 QY 11046 AGG3CCTATATGAGCTGACTGCTTGGCTGCGAGTCAGCAGCAGCACCT 11105 Db 961 GGCAGCTGTGGCGCTTCTGCACTGCGCTTCCTTTGGGGCCCTGGTACTC 1020 QY 3031 TTTCAGCAGCTGCACTGGTCTCTGCACTGCCGCTTCCTTGCGGCGCTGCTAC 1020 Db 1395 TTCAGGAACTCTTCACTCTGATGAGACATACTCTGCGACCTGGAGAC 1454 QY 11106 TTTCAGCAGCTGCACTGGTCTCTGCACTGCCGCTTCCTTGCGGCGCTGCTAC 11165 Db 1021 TTTCAGCAGCTGTGGCTTCTGCACTGAGCTGAGCTGAGCTGAGCTGAGC 1080 QY 3091 CAGTGGCCCTCCCTCAGGGAGTATCCAGGGAGGAGCTGAGCTAAGAGGAC 3150 Db 1455 ACCTTCGCGCAGGCCCHNGTGGCCACTCCACCTCCAGGCACTGGAGAC 1514 QY 11166 CAGTGGCCCTCCCTCAGGGAGGCACTCCAGGGAGGAGCTGAGCTGAGC 11225 Db 1081 ACCTTCGCGCAGGCCCHNGTGGCCACTCCACCTCCAGGCACTGGAGAC 1140 QY 3151 ACATGGCAACTCTG-CCTTCCCTCCGACAGGCCATACCTCTAATAGAGCAGTGA 3209 Db 1515 GAGCTGGGACGCCAGGGGAGGAGCCCTGGCCNAGGGGAGGAGGCCAGGCC 1571 QY 11226 ACAATGGCACCTCTGCCCTCCCTCCGACAGGCCATACCTCTAATAGAGCAGTGA 11285 Db 1141 GAGCTGGGACGCCAGGGGAGGAGCCCTGGCCNAGGGGAGGAGGCCAGGCC 1197 QY 3210 GACCCAGGGGGGGGCCACCCAGGGAGCTATGCCCTTCCTCCCTGCCGAC 3269 Db 11286 GACGCCA---GGTGGGCCACCCAGGGAGCTATGCCCTTCCTCCCTGCCGAC 11341 QY 3270 ACTCTCATGCCCTTCCTCGTCTCTCTCTAGCAAGGCCCTGCGGCCACCCTGCTGT 3329 Db 11342 ACTCTCAIGTCCCCTCCCTCTCTCTCTCTCTAGAACGCCCTGCGGCCACCCTGCTGT 11401 QY 3330 CCTCTGGATGGGATCTCTCACCCCTCTAGGCACTGCCCATCTGGGAGA 3389 Db 11402 CCTCTGGATGGGATCTCTCACCCCTCTAGAACGCCCTGCGGCCACCCTGCTGT 11461 QY 3390 ATATAGGATAGACACTGGACATGCCCATCTGGGAGCACCCTGGGAGA 3449 Db 11462 ATATAGGATAGACACTGGACATGCCCATCTGGGAGCACCCTGGGAGA 3389 QY 3450 ATCTCTGGAGGGGGCGCGC-GCCCACTTCCTCTCGTCACTGACACTGACACTG 3449 Db 11522 ATTCCTGGACAGGGGGCTGGGCCCTCACCTCTCTCTGACACACTGACACTG 3508 QY 3509 TGCTTGAGAATCTGGGGTGGAGGACAGAGAACCTGGGGCCACTGGGAGA 3568 Db 11582 TGCTTGAGAATCTGGGGTGGAGGACAGAGAACCTGGGGCCACTGGGAGA 11641 QY 3569 CTCTCTGACTGTGCTCACTGAGCTTGCTGCTCTCTCTCTCTGACACTGACACTG 3628 Db 11642 CTCTCTGACTGTGCTCACTGAGCTTGCTGCTCTCTCTCTGACACTGACACTG 11641 QY 3629 GGCGGTACCCCCCCCCAGCCCTCAAGTC-ACCCACTPCCACTGAGCTTGTAGCT 3687 Db 11702 GGCGGTACCCCCCCCCAGCCCTCAAGTCACCCCCCACCTCCACCTGAGCT 11701 QY 3688 ARACTCTCTAACCTATACCTTCTGTTGAGTAATTTGGATTGGGGAGAGG 3747 Db 11762 ARACTCTCTAACCTATACCTTCTGTTGAGTAATTTGGATTGGGGAGAGG 11821 QY 3748 GAGCAAAGGCCATAGCTTGGGGTGGACATCTCTAGTGTGCTGCCACATTT 3807 Db 10746 GGGGAAGTCTACGACTGGAGCTGAGCTGGGGCTTGTGAGCTGGAGGCT 10805 QY 11822 GAGCAAAGGCCATAGCTTGGGGTGGACATCTCTAGTGTGCTGCCACATTT 11821 Db 2849 GATGCTCTGAGGCCAGCCCTTGGCAGCTACGGAGGAGCTCATCGAGAC 2908 QY 3808 CTATACTACTGGGGTGTGACATTGTGGAGGAGACAGACAGATTACATA 3867 Db 10806 GATGCTCTGAGGCCAGCCCTTGGCAGCTACGGAGGAGCTCATCGAGAC 10865 QY 11882 CTATACTACT-GGTGTTGACATTGTGGGGAGGAGACAGATTACATA 11940 QY 2909 GAGGGACTCTCGGGGACCAAGGGGGGG 2936 Db 3868 TATGGACTCTGAGGCAATTAACTCCCTGACTAGGAGGAGATAAAGGTTG 3927 QY 10866 GGGGGAGTCTCCGGGACCAAGGGGGGGAGCTGAGAGCTGAGCT 10925 Db 11941 TATGGACTCTGAGGCAATTAACTCCCTGACTAGGAGGAGATAAAGGTTG 12000 QY 2937 3928 AGTTCCAC 3937 Db 10926 CGAGNCGGGGACAGAGGGGAGCTTCTGAGGAGTAAAGATAATGTC 10985 QY 2937 - CAGGTGACTCTGTCGGGGCTCTGCGCTGCGCT 2970 Db 10986 TGACTCTAACCAACACTTCCNAATNCAGGGTAGCTCGTCCGGGCTCGCCGC 11045

RESULT 6
US-09-880-107-3369
; Sequence 3369, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Gene Logic, Inc.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 3369
; LENGTH: 12010
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 048705
; NAME/KEY: unsure
; LOCATION: (1)-(12010)
; OTHER INFORMATION: n = a or c or g or t
; US-09-880-107-3369

Query Match 24.0% Score 950; DB 10; Length 12010;
Best Local Similarity 89.7%; Pred. No. 1 5e-160; Mismatches 5; Indels 126; Gaps 6;
Matches 1139; Conservative 0; Mismatches 5; Indels 126; Gaps 6;

QY 2789 GCGGAAGTCTAGGAGCTGGAGCTGGAGCTGGCTTGTGGAGGTGCT 2848
Db 10746 GGGGAAGTCTACGACTGGAGCTGAGCTGGGGCTTGTGAGCTGGAGGCT 10805
QY 2849 GATGCTCTGAGGCCAGCCCTTGGCAGCTACGGAGGAGCTCATCGAGAC 2908
Db 10806 GATGCTCTGAGGCCAGCCCTTGGCAGCTACGGAGGAGCTCATCGAGAC 10865
QY 2909 GAGGGACTCTCGGGGACCAAGGGGGGG 2936
Db 10866 GGGGGAGTCTCCGGGACCAAGGGGGGGAGCTGAGAGCT 10925
QY 2937 3928 AGTTCCAC 3937.

Db 10926 CGAGNCGGGGACAGAGGGGAGCTTCTGAGGAGTAAAGATAATGTC 10985
QY 2937 - CAGGTGACTCTGTCGGGGCTCTGCGCTGCGCT 2970
Db 10986 TGACTCTAACCAACACTTCCNAATNCAGGGTAGCTCGTCCGGGCTCGCCGC 11045

RESULT 7
US-09-35-915-5
; Sequence 5, Application US/09355815
; Publication No. US20030070184A1

STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DO/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/158,722
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/456,647
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 08/237,401
 FILING DATE: 02-MAY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/884,486
 FILING DATE: 15-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Wetherell Ph.D., John R.
 REGISTRATION NUMBER: 31,678
 REFERENCE/DOCKET NUMBER: 07251/007002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 688-5070
 TELEFAX: (619) 688-5099
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3120 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 IMMEDIATE SOURCE:
 CLONE: Tyro 10
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 485..3047
 US-09-158-722-19
 Query Match 16.1%; Score 639.8; DB 9; Length 3120;
 Best Local Similarity 56.5%; Pred. No. 3; Se-172;
 Matches 1552; Conservative 0; Mismatches 987; Indels 210; Gaps 11;
 Db 509 CTGGCTCTGCTCTGCTCTGCTCATCTGGTCTCGCAAAAGCTCAGTTATCCAGC 568
 Qy 408 AGTCGCCGATAGCCCTGGGATCGAGGACCCAGATCCAGACATGAGATCTGCT 467
 Db 569 ATATGCCGCTATCTCTGGCATGTCAGGAGCCATTCAGATGAGACATCAGCC 628
 Qy 468 TCCAGCTCTGGTCACTGCCTGGACTGAGCCGGAGATCCAGGAGCTGGGG 527
 Db 629 TCAACTCAGGGTCAAGATCCAGGCTGGGAGAATATGGGAGCTGGACTCTGAGAGGA 688
 Qy 528 GATGGGCCCTGGTCCGGCCGGGGGGGTTCCTCAAAGG---GGAGGAGTACTTGAG 584
 Db 689 GATGGAGCCCTGGTCTGAGATTCCAGTGCAGGAACTGAGGAAATTCTCGAG 748
 Qy 585 GTGGATCTAACAGCTCCACTGGGGCTTGGGGCACCCAGGAGCCATGCCGGG 644
 Db 749 ATTGACTTGTGCAACCTACTTATCACTCTTGAGGGGGACCCAGGGCCATCGAGG 808
 Qy 645 GGCTCTGGCAAGGAGCTCTCCGGAGCTACGGGCTGGTACTCCGGGATGGTCCCGC 704
 Db 809 ATTGACTTGTGCAACCTACTTATCACTCTTGAGGGGGACCCAGGGCCATCGAGG 868
 Qy 705 TGGATGGGCTGGGAGGACCCCTGGGCTGGGGATCTCAGGAGTATGAGGACCTGTGAG 764

Db	869	TGGATCTCTGGCGTAACCGCATGGAGCAGGGCTGATGAAACAGTAACTTAT	928	Oy	1839	CTGGCTCCATCCAGCCAACGCCCTCTGCCCTCTGCCAACACTACGCCGRCCCCCCTGAGGC	1898
Oy	765	GGATGGGGCTGAGGAGCTTGCCCCCATGGTGGCGACAGTGTGCTCTACCC	824	Db	1943		1948
Db	929	GATGTTATCTGAGGACTGGCCACCCATGTCGCAAGATTTGTCTGCTTATCCCA	988	Oy	1899	CCGGCCCCCAACCCGCTGGCCAAACCAACACCGGCCAACAGGGCTACAGGGAC	1958
Oy	625	CAGCTGAGGGCTCATGGTGTGCTGGGGTAGGGCTATGGCTCATGGCTGCCCCTGGAG	884	Db	1949	-----	1983
Db	989	GTCATGACCTCCATGACGCTGAGGGTTGGCTTATGGTGTGCTGAGGCTA	1048	Oy	1959	TATWGGACTGTGAGAACCCAGGGCCCTGGGGAGAGAATGATTTCCTGAGG	2018
Oy	885	GATGGACTCTGCTTACACGCCCTGGGGAGAGCAGCTGAGCAGCTGAGG	939	Db	1049	GATGGCTTGTGATCTACATGTCATGGCTGAGCAGCTGAGCAGCTGAGG	1108
Db	1049	ATGCTGGCTTGTGATCTACATGTCATGGCTGAGCAGCTGAGCAGCTGAGG	1108	Oy	940	-CGTGTACCTAACGACTCACGCTTACCTATGGCTGAGGCTTATGGTGTGAGG	998
Oy	1169	--CTAGGCCAGTTGACTGATGAGTATGGAGTATCCGGCTGTGAGTATGG	1225	Db	1109	ATCATTTATCTGATGTTCTGAGTGGAGCTGTTGGACAGGATGACTGAGG	1168
Oy	1059	CTGGGCTCTGGCAGGCCATGACTATGCTGGATGGAGAACACAGGTTCTCAGT	1118	Db	999	GCTCTGGGCCAGCTGGGATGGCTGAGCTTACGGAGAGTCAGAG	1058
Db	1226	TACACGTTGGCTGGCTGAGTACTGCTGGATGGAGAACAGGCTTACCAAGGG	1285	Oy	1119	TATGTGGAGATGGAGTTGAGTTGACGGGCTGAGGCTTACGGCTAGG	1178
Oy	1119	TATGTGGAGATGGAGTTGAGTTGACGGGCTGAGGCTTACGGCTAGG	1178	Db	1286	TTCATGAGATCATGTTGATGTTGACGGAACTCAGGAATTCAGTGGAGG	1345
Db	1179	TCTAACACATGACACGGCTGGAGGCCCTGGCTGGCTGGATGGAGG	1238	Oy	1179	TCTAACACATGACACGGCTGGAGGCCCTGGCTGGCTGGATGGAGG	1238
Oy	1346	TGCAACACATGTTGCTTAAGGTGTGAGATTAACTGGAGTCTGCTG	1405	Db	1406	TGG---AAGCCGGCTGGAGGCCCTGGCTGGCTGGCTGAGGAT	1462
Oy	1239	CTGGGCCCTGGCATGGCTGGAGGGAGGCCATGGCCACACCTAGGGG	1298	Db	1359	CACTGCGCTCTCTGGAGGCCCTGGCTGGCTGGCTGAGGAT	1418
Db	1463	GTGAACCCCACTGGGGTTGTACGGTGGCCCTCACCCAGATGGCAAG	1522	Oy	1523	AAGTGCCTATACATTGCGCACAGCTGGATGATGTCAGTTCATCA	1582
Oy	1419	GATGGGTGACAATTCCCTGGGACTGGGGACCTGGGGAGCTGGGG	1478	Db	1583	GATGGGTGACAATTGATGAGTACACTCTGGAGCTTCCACATCT	1626
Db	1583	GATGGGTGACAATTGATGAGTACACTCTGGAGCTTCCACATCT	1626	Oy	1479	CGCCCTGGCCACCTCCACCAACTCTGAGCTTCCACATCT	1538
Oy	1627	-----TATGGCACCCACACCTATGAT	1648	Db	1539	CCCGGGCCAAAGGCCGAGGGAGGCCCTCATGGCTGGCTGGCTGG	1598
Db	1649	ATCCGGCTCTGGCTCTCATGGCTGGCTGGCTGGCTGGCTGG	1708	Oy	1599	ATCCGGCTCTGGCTCTCATGGCTGGCTGGCTGGCTGGCTGG	1658
Oy	1709	ATCTCATCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1768	Db	1709	ATCTCATCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1768
Db	1649	CCCATGCTTAAAGTGTGATGATGACACCTGGATCTGTGTTGTTG	1708	Oy	1659	CTCAGCAAGGCTGAAGGGGGTGGAGAGGAGCTGAGGTGACCT	1718
Oy	1769	CTGAGAACACCTTCACGGGGATCTGGATGATGAAATGACAGT	1828	Db	1769	CTCAGCAAGGCTGAAGGGGGTGGAGAGGAGCTGAGGTGACCT	1828
Db	1719	GGGGACACTACCTCATCACACGGCCCTAGGTGAGGAGCTGAG	1778	Oy	1829	AGCAGTCTCAGCATGTCATACACCCGCTCTC-----ATACCAAGT	1882
Oy	1779	CCCCGGCCCTGGGAACTGGCCACTCTGGCTGGCTGGCTGG	1838	Db	1883	TCCAATCTACTATGATGAACTCTCCCTCGCCCTGACTACCAG	1942

RESULT 13
 QY |||||||GCCTCACTGGCTTCCTCCATCACTGAAACACTGGACCTGGGTAGCC 3639
 Db 61 GTCCCTACACTGGCTTCCTCCATCACTGAAACACTGGACCTGGGTAGCC 120
 QY 3640 CGCCCCAGCCTAGTCACCCCACTGCCACTTGCGACTCTGAGCTAGAACTTCCTTA 3699
 Db 121 CGCCCCAGCCTAGTCACCCCACTGCCACTTGCGACTCTGAGCTAGAACTTCCTTA 180
 QY 3700 AGCCTATCTGTTCTGAGTAAATGGATTGGGGAAAGAGGGAGAACGCC 3759
 Db 181 AGCCTATCTGTTCTGAGTAAATGGATTGGGGAAAGAGGGAGAACGCC 240
 QY 3760 ATAGCCTCTGGGTGGACATCTAGTAGTGCGCACATGTTCTATACCT 3819
 Db 241 ATAGCCTCTGGGTGGACATCTAGTAGTGCGCACATGTTCTATACCT 300
 QY 3820 GGGT 3824
 Db 301 GGGT 305

RESULT 14
 US-09-294-093B-1691
 Sequence 1691, Application US/09294093B
 GENERAL INFORMATION:
 PATENT NO. US2010051335A1
 APPLICANT: Lagudi, Raghunath, V.
 APPLICANT: Sherman, Bradley, K.
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
 CURRENT APPLICATION NUMBER: US/09/294,093B
 CURRENT FILING DATE: 1999-04-16
 PRIOR APPLICATION NUMBER: 60/082,567
 PRIOR FILING DATE: April 21, 1998
 NUMBER OF SEQ ID NOS: 6207
 SOFTWARE: PERL, Program
 SEQ ID NO: 1691
 LENGTH: 289
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: n = A,T,C or G
 LOCATION: (1)-(470)
 US-09-918-995-9027
 Query Match 6.4%; Score 255; DB 9; Length 470;
 Best Local Similarity 98.1%; Pred. No. 1.4e-62; Matches 258; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3677 GCTCTGTAGCTAGACTCTCTAAGCTTATAGTTCTGTGGAGTAATATGGATGG 3736
 Db 31 GCGTATCTCTAGACTCTCTAAGCTTATAGTTCTGTGGAGTAATATGGATGG 90
 QY 3737 GGGGAGAGGAGGAGCAAGGGCCATACGCCATGGGTGGAGACATCTCTAGCTAGCTAGTGCC 3795
 Db 91 GGGGAGAGGAGGAGCAAGGGCCATACGCCATGGGTGGAGACATCTCTAGCTAGTGCC 150
 QY 3797 CATTGATTTCTATACCTGGTTGACATTGGGGAGACACAGATT 3856
 Db 151 CATTGATTTCTATACCTGGTTGACATTGGGGAGACACAGATT 210
 QY 3857 TTACACTATATAATGGACTACTTGAGGCAATTAAATCCCTGACTAGGCAATAAT 3916
 Db 211 TTACACTATATAATGGACTACTTGAGGCAATTAAATCCCTGCACTAGGCAATAAT 270
 QY 3917 AATAAAGTTGAGTTCCACA 3939
 Db 271 AATAAAGTTGAGTTCCACA 293

RESULT 15
 US-09-960-352-726/c
 Sequence 726, Application US/09960352
 PATENT NO. US20020137159A1
 GENERAL INFORMATION:
 APPLICANT: Warren, Wesley C.
 APPLICANT: Tao, Nengbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Nagappan
 TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION ANE
 TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
 FILE REFERENCE: 16511_006737-21(1028)C
 CURRENT APPLICATION NUMBER: US/09/960,352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO: 726
 LENGTH: 387
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 04-L11188-016-01-E1-A7
 US-09-960-352-726

Query Match	Best Local Matches	Local Similarity	Score	DB 10:	Length
	3453	CCTGGAGAGGTGGCGCAG--GCCCACTTCCTCTCTCCCTGTCACACTTGACCCCCACTG	82.5%	Pred. No. 2	Score 232.8; DB 10: length 387;
	386	CCTGGAGAGGTGGCGCAG--GCCCACTTCCTCTCTCCCTGTCACACTTGACCCCCACTG	0	Mismatches	Indels 5; Gaps 4;
	3511	GCTGAGAATCTGGG-GTGAGGAGGACAGAGGAGGAAATGTTCTTGCCRC	3510		
	326	GCTGAGAATCTGGGAGGTGAGGAGGACAGAAAGGGGAAGGGGTTCCTGATCTC	3569		
	3570	TCCGTACTGTGCTCACGCTGGGCTCTCTCCCTCATCACCTGAAACACTGGACCTG	327		
	266	TCCGGAAATTGCCCTCAGCTTGGCTTCCTCTCATCTCTGAAACACTGGACCTG	3629		
	3630	GGGGT-AGCCCGGCCGACCCCTCAGTCACCCACTTCCACTTGAGCTGTAGCTA	207		
	206	GGGGTGTACCTAACCCCCACCCCTCAGCTCCACCTGCTCCACCTGCGTGTACCTA	3688		
	3689	GAACCTCTTAAGCTTATAGTTCTGGGAGTAATATGGATT-GGGGGAAAGAGG	147		
	146	GAACCTCTTCAAGCTGTAGTTCTGTGGATAATGATGGATTGGGGAAACAGA	3747		
	3748	GAGCAACGCCCATGCCTGGGGTGTGACATCTGTGTGAGCTGCACATGTATT	87		
	86	GAGCAACGCCCTGGGCCCTGGGGTGTGACATCTGTAGCTGCACATGTATT	3808		
	26	CTTAATACCTGGGGTTGTA	3829		
		CTTAATACCTGGGGTTGTA	27		

Search completed: May 30, 2003, 16:10:26
Job time : 506 secs